Internship : Development of a user-friendly pipeline for Graph neural network based biomolecule trajectories analysis

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Scientific background

Single molecule localization microscopy allows one to observe the movement of individual proteins at the membrane of cells. Proteins are the elementary actors of virtually every process happening in the cell, and the quantitative analysis of their dynamics already provided valuable insights about a wide range of mechanisms [1, 2].

In the lab, we're developing innovative analytic tools to quantitatively characterize biomolecule trajectories, relying on neural networks and semi-supervised learning. In particular, we're developing a method to characterize random walks using graph neural networks [3].

Numerous processing steps are required to extract trajectories from raw images acquired by the microscope's camera, making the analysis complex and challenging to reproduce. To be beneficial to the community of researchers interested by its capabilities, our novel type of analysis should be integrated to a pipeline usable by non-developers. Such an integration would be highly valuable and potentially lead to novel scientific findings.

Internship description

The intern will start by familiarizing (him/her)self with the existing set of tools available for super-resolution microscopy analysis as well as deployment of neural networks, and with the specifics of the methods we implement at the lab. Then, in collaboration with Hippolyte Verdier (PhD student) and François Laurent (one of the PI of the lab), he'll design and implement a pipeline allowing experimentalists to use our tools to perform analyses. This will include deploying deep-learning methods into a "production" setting.

Intern's skills

- Required :
  - Python
  - Deep learning
- Valued :
  - Experience in software development
  - PyTorch

Logistics

Location : Institut Pasteur (Paris 15$^{\text{ème}}$)
Salary : ≈500 euros
Duration : 3-6 months

References

1. Knight, S. C. *et al.* Dynamics of CRISPR-Cas9 genome interrogation in living cells. *Science* **350,** 823–826 (2015).
2. Floderer, C. *et al.* Single molecule localisation microscopy reveals how HIV-1 Gag proteins sense membrane virus assembly sites in living host CD4 T cells. *Scientific reports* **8,** 1–15 (2018).
3. Verdier, H. *et al.* Learning physical properties of anomalous random walks using graph neural networks. *Journal of Physics A: Mathematical and Theoretical* (2021).